Public Health Watch

A BI-MONTHLY PUBLIC HEALTH NEWSLETTER OF THE
METROPOLITAN HEALTH DEPARTMENT OF NASHVILLE AND DAVIDSON COUNTY, TENNESSEE

Volume 4, Number 6 ISSN - 1009 - 7423 **September/October 2000**

Why Genetic Competencies in Public Health?

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Genetics might be to public health in the 21st century what infectious disease was in the 20th century.

When we say "public health", we normally think about "prevention". Traditionally, public health focused on (1) modifiable risk factors for diseases such as cigarette smoking, alcohol consumption, obesity, physical inactivity, and high-risk sexual behaviors; (2) preventive interventions such as immunization, restaurant inspections, and maternal and child health services; and (3) screening for disease precursors such as hypertension and cervical dysplasia. Such risk factors and precursors for diseases usually become apparent in adolescence or later in life and are often amenable to preventive measurement[1]. Genetic factors, however, have been viewed as intransigent, immutable, and innate. How can genetics and public health be integrated? Why do we need genetic competencies in public health?

To answer these questions, we may need to re-examine our perspective. As we enter the 21st century, health care is undergoing phenomenal changes driven, in part by the Human Genome Project and accompanying advances in human genetics[2]. To have a genetics-driven health care perspective, it is appropriate to review some basic genetic concepts, to understand "old" genetics, to comprehend "new" genetics, i.e., genomic medicine and genomic public health. Only then will we realize that with acceleration of the discovery of human genetic variation and associated diseases in the next few years, public health professionals will not only be confronted with but will help develop, analyze, and disseminate a large body of scientific information that will guide public health actions.

What is genetics?

Genetics is the scientific study of heredity: how particular qualities or traits are transmitted from parents to offspring. Some basic genetics' terms such as genome, DNA (deoxyribonucleic acid), genes, and chromosomes are reviewed as follows[3].

Inside the nucleus of every one of the billions of cells that make up a human being is a genome, or DNA blueprint, for that individual.

DNA is a vast chemical information database that carries the complete set of instructions for making all the proteins a cell will ever need. DNA exists as two long, paired strands spiraled into the famous double helix. Each strand is made up of millions of bases. If we could think of DNA as a necklace for a moment, this necklace is made up of 3 billion pearls in four different colors, representing four different chemical bases (adenine, thymine, cytosine, and guanine). The order of the bases determines the information available, much as specific letters of the alphabet combine to form words and sentences.

Each cell has 46 molecules of double-stranded DNA. Each DNA molecule is made up of 50 to 250 million bases housed in a chromosome. The DNA in each chromosome constitutes many genes (as well as vast stretches of noncoding DNA, the function of which is unknown).

Genes are working subunits of DNA. A gene is any given segment along the DNA that encodes instructions that allow a cell to produce a particular protein. Proteins are the

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building blocks of all human functions and of characteristics like eye color. There are between 50,000 and 100,000 genes, and every gene is made up of thousands, even hundreds of thousands, of chemical bases.

Human cells contain 46 chromosomes, divided equally into two sets. One set is inherited from the mother and the other set from the father. Mature sperm and egg cells carry a single set of 23 chromosomes. Each set has 23 single chromosomes - 22 autosomes and a X or Y sex chromosome. Females inherit a X from each parent, while males get a X from the mother and a Y from the father. (Figures 1, 2)

Figure 1. Cell, Chromosome, and DNA

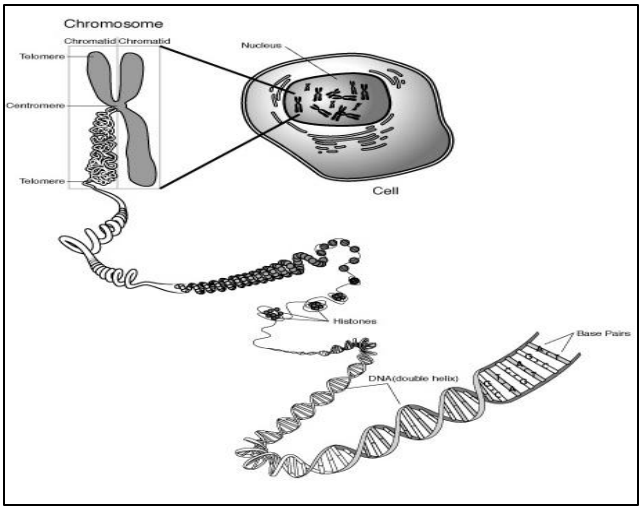
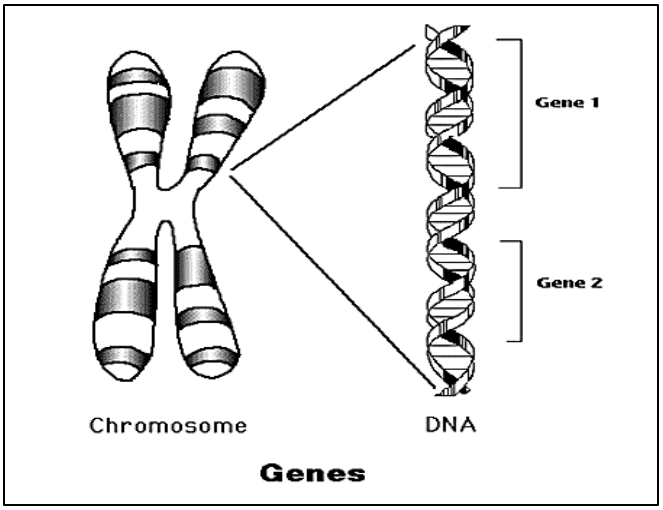


Figure 2. Cell, Chromosome, DNA, and Gene



Source: http://www.accessexcellence.org/AB/GG/

On June 26, 2000, biologists J. Craig Venter and Francis S. Collins announced that their two research groups has mapped[a] the human genome: a strand of DNA in which 3 billion chemical parts spell out the genetic code of life[4]. This breakthrough signifies a new era in genetics. To reflect the significant impact of the Human Genome Project on genetics and on our life, genetics before the Human Genome Project's breakthrough is considered the "old" genetics". The "new" genetics was born after the successful Human Genome Project[6].

What is "old" genetics?[6]

"Old" genetics study conditions completely caused by: 1) chromosomal disorders (extra or missing whole/part of a chromosome) and 2) a single gene disorder (mutation). Examples of chromosal disorders are Down syndrome (an extra copy of chromosome 21) and Turner syndrome (absence or defect of the second X chromosome). Cystic fibrosis (a deficient protein) and phenylketonuria (a deficient enzyme) are due to gene mutations.

The conditions studied by "old" genetics are of great importance to affected individuals and their families. However, even when added together, these conditions are relatively rare. Most people are not directly affected. This limits genetics to a relatively small role in health care and in society. Due to limited number of persons affected, "old" genetics care is usually provided by medical geneticists and genetic counselors.

Because of "old" genetics' small impact on population health, the public's interest is limited and research is relatively not well funded. Consequently, genetics in the past two decades contributed more toward improvement of lab tools than toward improvement of population health.

What is "new" genetics?[6]

"New" genetics is based largely on knowledge from the Human Genome Project - an international scientific collaborating project. As we mentioned previously, the human genome consists of about three billion chemical bases. It would fill 150,000 telephone book pages with A's, C's, G's, and T's. Many diseases are associated with a single variation in the three billion bases - one letter in the 150,000 pages.

The Human Genome Project is of revolutionary significance in terms of providing a foundation in understanding the fundamentals of biology and the complexity of life. However, the Human Genome Project is "only" about the human genome

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[a] The Human Genome Project will result, as early as 2003, in a complete and accurate DNA sequence representing the genetic blueprint and evolutionary history of the human species. A "working draft" of this "book of life" may be available as early as 2001[5].

sequence - the alphabet, the telephone book. It is important but of little influence alone. It will help us to understand the diseases, but we still need to find ways to conquer the diseases. In other words, the real impact on peoples' lives comes from figuring out how words and sentences are formed and then creating new poetry, or how the telephone book is used to find critical persons and to engage them into communications and actions.

"New" genetics study conditions partly (1) caused by mutation(s) or polymorphism(s) in gene(s), e.g., colon cancer, breast cancer, diabetes, Alzheimer's disease, and many others, or (2) prevented by mutation(s) or polymorphism(s) in gene(s), e.g., HIV (CCR5), cancers, diabetes, and many others.

These conditions are common, directly affecting virtually everyone. Since the conditions are common, "new" genetics care will be supplied primarily by primary care providers from many health disciplines, with occasional involvement of medical geneticists, genetic counselors, and other medical specialists. Therefore, "new" genetics will play a larger role in health care and in society.

Public health implications

As of 1999, more than 10,000 genes have been discovered and catalogued. Tests for more than 600 gene variants are already available in medical practice. More than 4,000 diseases are known to have genetic components. Moreover, it is now known that alterations in our genes play a role in such common conditions as heart disease, diabetes, and many types of cancer. Virtually all human diseases result from the interaction of genetic variation with environmental factors, such as behaviors and exposures[2]. (Figure 3)

Taking leading causes of death as the examples, in 1998 more than nine of the ten leading causes of global deaths[b] have genetic components, and more than nine of the ten leading causes of U.S. deaths[c] have genetic components.

However, most genetic components for the common diseases now identified are low frequency, high penetrance[d] alleles[e]. In other words, these genetic components are not common in the population, but if one has these genetic components, his/her likelihood of developing the disease is high. For example, BRCA1 and BRCA2 gene mutations are responsible for a small proportion of breast and ovarian cancer. The overall carrier frequency of BRCA1 gene mutations is estimated at 0.2% in the general U.S. population[8].

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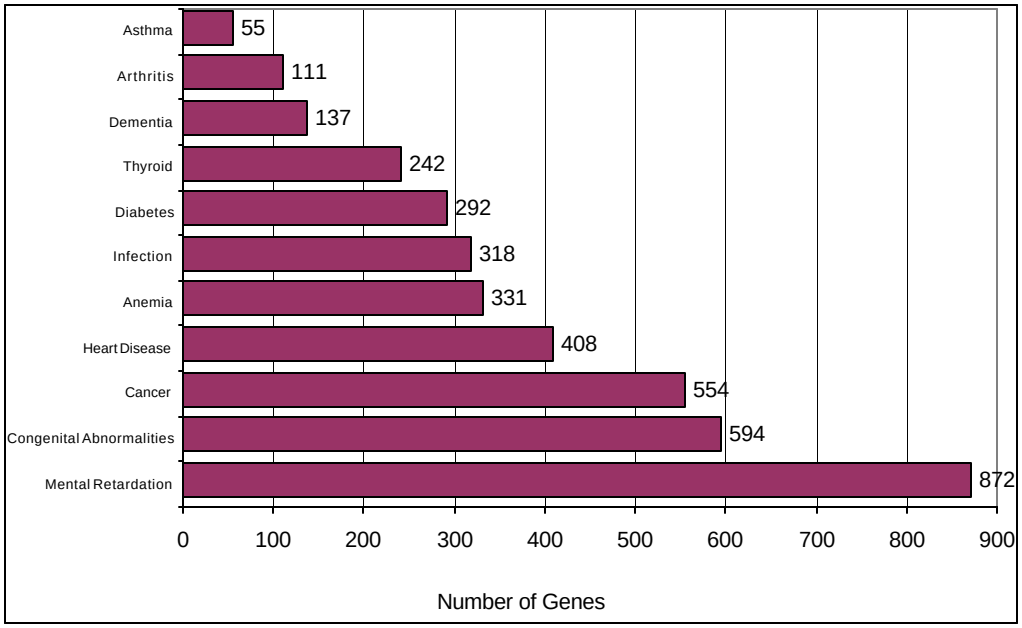
[b] The ten leading causes of global deaths in 1998 are heart disease, stroke, pneumonia, HIV/AIDS, Chronic Obstructive Pulmonary Disease (COPD), diarrhea, perinatal conditions, tuberculosis, lung cancer, and traffic accidents.
[c] The ten leading causes of U.S. deaths in 1998 are heart disease, cancer, stroke, COPD, unintentional injury, pneumonia/influenza, diabetes, suicide, kidney disease, and chronic liver disease.
[d] Penetrance: a term indicating the likelihood that a given gene will actually result in disease.
[e] Alleles: alternative forms of genes or genetic locus that differ in DNA sequence.

Figure 3. Number of Genes Reported to Increase Susceptibility to Selected Conditions



Source: Khoury MJ, Burke W & Thomson EJ. Genetics and public health in the 21st century. Oxford University Press, NY, 2000.

On a population level, most genetic contributions to common diseases are from high frequency, low penetrance alleles. In other words, these genetic components are common in the population, however, for those who have these genetic components, the likelihood of developing the disease is low. Examples are APC I1307K and colon cancer, and CCR5 and HIV/AIDS resistance[2]. The APC I1307K gene, present in 1 in 17 Ashkenazi Jewish people, has a weak association with colorectal cancer in that population. The Δ32 CCR allele is found in up to 20% of some northern European populations. Inconsistent associations have been observed with the Δ32 CCR gene and reduced heterosexual or vertical HIV transmission. From a public health point of view, identification of these high frequency, low penetrance alleles will have significant impact on population health.

The good news is that in the next few years, all of the 50,000 to 100,000 human genes will be identified. As these genetic contributions to more common diseases are identified, the underlying biochemical causes of major human diseases will be better understood, and the etiology of many other diseases will be determined, including "non-genetic" diseases. The "new" genetics will change health care by providing knowledge of individual genetic predisposition, creating pharmaco-genomics, allowing population based screening for genetic disorders.

Knowledge of individual genetic predisposition will allow individualized screening and individualized behavior changes. Pre-symptomatic medical therapies will be used, e.g., anti-colon cancer agents before colon cancer develops, anti-hypertensive drugs before hypertension develops.[6]

Pharmaco-genomics will allow individualized medication use based on genetically determined variation in effects and side effects. New medications for specific genotypic disease subtypes will be developed.[6]

Most important of all, emphasis will be on prevention rather than disease treatment. Finding the susceptibility genes permits those who have inherited them to avoid dangerous environments. For example, the person who knows he is genetically susceptible to coronary heart disease can be taught from a very early age to avoid high-fat foods, while the alcoholism-prone individual can be warned to avoid alcohol. Avoidance of risky environments could be taught early in childhood and thus would become a natural part of the individual's life style without the discomfort and difficulties of giving up cherished habits[7].

Early detection of host susceptibility also could alert parents and physicians to watch for symptoms of incipient disease in a child, so that treatment could begin before too much harm is done. For example, this early treatment might be possible to individuals with diabetes[7].

The above are the examples of prevention. The "new" genetics offers golden opportunities for public health professionals. The conditions to which people exhibit genetic susceptibility are so common that they will have great impact on population health and are of great public interest. Experts predict that genetics will be a focus for public health professionals. Genetics might be to public health in the 21st century what infectious disease was in the 20th century[6].

Furthermore, the "new" genetics will allow more genetic engineering against (and for) diseases and characteristics. The "new" genetics may include characteristics that most do not see as "diseases" and many do not see as innate. Examples are height, intelligence, sexual orientation, alcoholism, violence, happiness-sadness, confidence-anxiety, and altruism-greed[6].

The "new" genetics will also change our lives by allowing everyone to know their own (and maybe others) health and disease predisposition, by allowing everyone to know their own (and maybe others) "characteristics" predisposition. It may also change society through social stratification by genetic status, e.g., in employment or marriage. It increases opportunity for cloning and "private eugenics"[6].

All of these possibilities raise not only opportunities but also new concerns. The examples include discrimination against individuals and groups, genetic determinism, fairness in access to genetic information, confidentiality and privacy of genetic information, right not to know and not to act, appropriate informed consent process for genetic testing, and patenting and licensing of genetic information[6].

How do public health professionals prepare for genomic public health?

As the science of gene discovery matures, there will be an increasing role for public health in closing the gap between gene discovery and applications to prevent human diseases, especially adult-onset chronic diseases.

In the not too distant future, disease prevention and health promotion will routinely consider whether or not to use genetic information to help target intervention so as to maximize the benefit and minimize the cost and harm to individuals.[2] For this to occur, public health professionals need to learn to **"think genetically".** We need to know when genetic factors will play a role. We need to effectively use family history information and genetic testing. We need to learn how to explain genetics concepts to the community. We need to deal with "genetic risk" and genetic predisposition. We need to be aware of personal and societal impact of genetic information. We need to protect genetic privacy. We need to use genetics to individualize patient care and to promote health and prevent diseases and injuries.[6]

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We also need to help our community to prepare for the "new" genetics, to have understanding of the basics of the science of genetics, the eventual use of genetics in health care, how to deal with genetic risk and genetic predisposition, and the personal impact of genetics information.[6]

Therefore, we do need genetic competencies in public health.

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Note: *The author is a member of the epidemiology working team of the CDC Competencies for the Public Health Workforce: Integrating Genetics into Public Health Project.*

Acknowledgements*: The framework of "old' genetics, "new" genetics, genomic medicine, and genomic public health is based on a presentation titled " Genomic Medicine and Public Health." by Alan E. Guttmacher, MD, Senior Clinical Advisor to the Director National Human Genome Research Institute, National Institutes of Health. Yi-Wei Tang, MD, PhD, Medical Director of the Molecular Infectious Disease Laboratory at the Vanderbilt University Hospital reviewed the manuscript.*

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Metro Health Department Adopts Geographic Information Systems Technology

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A relationship between one's health and one's location has been well established. The depiction of these relationships with maps also has a long tradition, perhaps most notably including Dr. John Snow's now-famous mapping of a cholera outbreak in 19th century London that identified a strong spatial relationship between victims and a nearby public water pump. Here in the early 21st century disease mapping has been revitalized thanks in large part to computer technology and, more specifically, the development of *geographic information systems*.

> "A geographic information system (GIS) is a computer-based tool for mapping and analyzing things that exist and events that happen on earth."
> -Environmental Systems Research Institute, 1998

The above quote comes from the makers of the GIS software used by the Metropolitan Health Department of Nashville and Davidson County (MHD). Acquired by purchase and grant, the Engineering Services Division of MHD's Environmental Health Services Bureau has installed a suite of tools designed to monitor and analyze phenomena that occur on, above, or underneath the earth's surface impacting the environment of Davidson County and the health of its citizens. Furthermore, our Division is offering this capability to the other areas within MHD and to the local health community at large.

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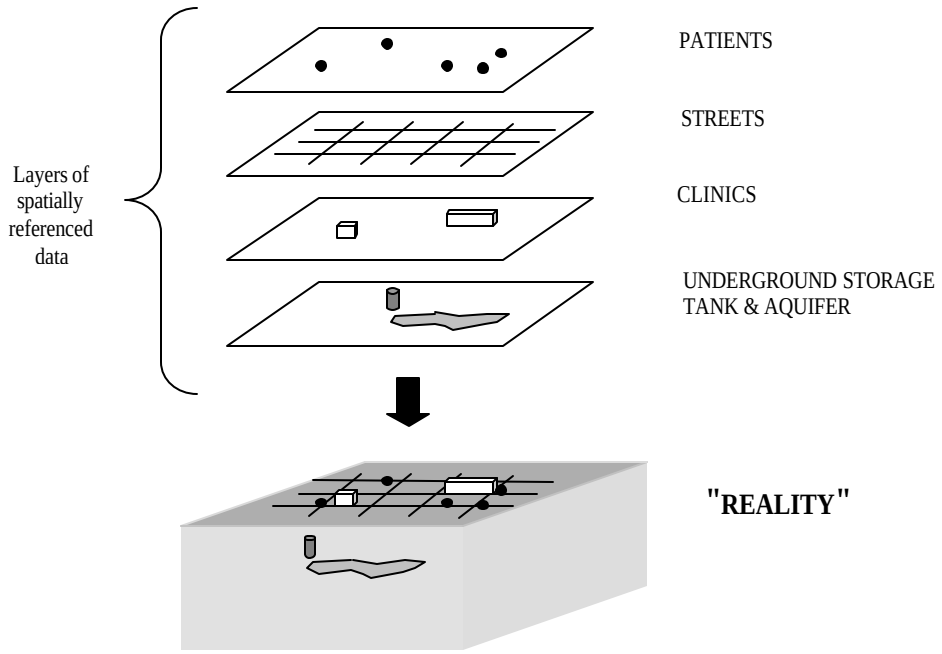
The essence of a computer-based GIS is its ability to store information utilizing standard database techniques with the inclusion of a spatial reference. Most often that spatial reference is stored as Cartesian coordinate data where real-world features are represented by a pair or pairs of numbers that are positions along X and Y axes. One well-known example would be the point at 0 degrees latitude and 0 degrees longitude, otherwise known as the intersection of the equator with the prime meridian that occurs in the Atlantic Ocean off the coast of Africa. A somewhat lesser known example would be X: -86.78, Y: 36.17 which occurs at the building housing the Tennessee State Capital. Items best represented by lines, such as streets and rivers, are stored as line segments with two pairs of X, Y coordinates indicating the endpoints of the segment. Finally, features that are shown by area are stored as a series of X, Y coordinate pairs where two pairs are identical. The two identical pairs "close the loop" and complete an outline of, say, a lake or a census tract.

Coordinate data alone would be enough to make pictures. However the analytical potential of GIS is realized when data describing the attributes of features are stored along with the coordinates and when similar features are grouped and stored in separate files that are treated as layers. In this manner certain phenomena can be selected, or queried, by the attributes associated with it and compared to other features stored in separate layers. Assuming the presence of relevant attribute data associated with the data layers depicted in Figure 1, one could query the GIS to identify all patients earning less than $20,000/yr. residing on Murfreesboro Road and more than 3 miles from a health clinic and less than 1 mile from a permitted underground storage tank.

One of the more popular features of a GIS is its ability to generate X, Y point locations based on a street address. In the past we have been limited to data at the county or, at best, the census tract level. Now however the MHD has the capability to analyze data by any geographic unit as well as the ability to identify localized clusters of activity that would otherwise escape detection (Figure 2). Another important feature is the ability to model scenarios to predict outcomes. Emergency response is one area well suited for GIS. For example, a hypothetical toxic spill could be plotted and analyzed against topographical and hydrological data to predict a contamination pathway. In addition, demographic data could be brought in to help forecast likely exposure rates. GIS is also an excellent management tool that assists in the routing of caseworkers, clinic siting, and other means of efficient resource distribution.

Figure 1: Spatial Data As "Layers"



Source: Environmental Systems Research Institute, 1998

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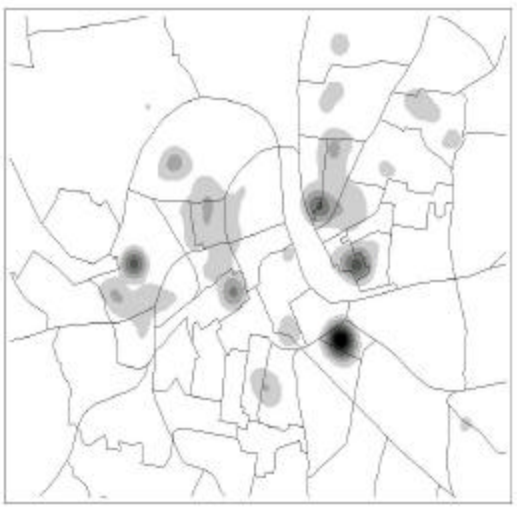
Figure 2: Incidence "Hotspots" and Downtown Nashville Census Tracts



Indeed, GIS is a powerful and complex new tool. However, more work remains before its integration with our organizational structure and workflow is complete. Many thanks are owed to the Metropolitan Planning Department, for guidance as well as for data. MHD looks forward to continued cooperation with the Metropolitan Planning Department and with local health, medical, and community groups in leveraging GIS in the promotion and protection of our citizens' health and environment. To learn more about GIS, try these two websites: 1) www.gis.com and 2) www.cdc.gov/nchs/about/otheract/gis/gis_home.htm. For comments, concerns, or suggestions please contact Jim Jellison at (615) 340 – 5326 or jim_jellison@mhd.nashville.org.

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Two Major Changes in Mortality Data

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Within a few months, the 1999 death data will be released to the public. Several big changes in mortality statistics will be noticeable. For example, there may be a substantial decrease in deaths due to pneumonia and a significant increase in deaths due to Sudden Infant Death Syndrome (SIDS). The age-adjusted death rate for heart disease may double. … Are these increases and decreases real?

The good news is that the increases/decreases in some death statistics are NOT REAL but are due to two methodological changes in the United States regarding mortality data. The two major changes in mortality statistics effective in 1999 data are:

1. Implementation of ICD-10, and
2. Implementation of the new standard population for age-adjusting death rates.

For your information, I will summarize these two changes and their potential impact below, based on information obtained from the National Center for Health Statistics' (NCHS) 2000 Data User Conference.

Change 1: Implementation of ICD-10

The International Classification of Diseases (ICD) is a classification system developed collaboratively between the World Health Organization (WHO) and ten international centers so that the medical terms reported by physicians, medical examiners, and coroners on death certificates can be grouped together for statistical purposes. ICD-10 is the newest revision of ICD. It replaces the ICD-9 that was used with 1979-1998 data. ICD-10 promotes international comparability in the collection, classification, processing, and presentation of mortality statistics.

Use of the year 2000 population standard will affect trends in age-adjusted rates for certain causes of death and will narrow race differentials in age-adjusted death rates.

Why do we use ICD-10?

The United States is required to use the ICD for the classification of diseases and injuries under an agreement with WHO that has the force of an international treaty. By using the ICD, the U.S. collects, processes, and presents mortality data in a similar

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way to other countries around the world. This permits comparison of data across countries. Periodically, new revisions are developed to reflect advances in medical sciences.

What are the effects of changing to ICD-10?

ICD-10 affects the classification, processing, and presentation of mortality data. Some titles have changed; the total number of categories has doubled as a result of the addition or deletion of terms used to describe diseases or conditions; the transfer of certain diseases from one section to another reflects new discoveries and advances in knowledge on the nature or cause of particular diseases; and the addition of separate categories identifies specific diseases or particular complications of certain diseases that are of growing interest. Additionally, the codes associated with each title have been converted from numeric to alphanumeric entities. The ICD rules for processing mortality data are generally similar but account for some changes observed in mortality statistics. The tabulation lists used to present mortality data in routine tables have been revised to reflect the new classification.

How does ICD-10 compare to ICD-9?

Compared with ICD-9, ICD-10 has

- expanded detail for many conditions (e.g., viral hepatitis has been expanded from ICD-9 070, a single 3-digit category, to ICD-10 B15-B19, five 3-digit categories)
- transferred conditions around the classification (e.g., hemorrhage has been moved from the circulatory chapter to the symptoms and signs chapter)
- used alphanumeric codes instead of numeric codes (e.g., code for diabetes mellitus was 250 in ICD-9 and is E10-E14 in ICD-10)
- modified coding rules (e.g., the "Old pneumonia, influenza, and maternal conditions" and "Error and accidents in medical care" coding rules have been eliminated)
- modified the tabulation lists (e.g., the US' ICD-10 113-cause list replaces the US' ICD-9 72 cause list)

The results of the preliminary comparability study (examines similar categories in successive revisions to measure the extent of breaks in trends caused by introducing a new ICD revision) is expected to be available from the National Center for Health Statistics by fall 2000.

What are examples of expected changes to mortality statistics?

Example 1: Substantial decrease in deaths due to pneumonia. This is due to changes in coding rule 3 in which pneumonia is a direct sequel to many more conditions in ICD-10.

Example 2: Increase in deaths due to Sudden Infant Death Syndrome (SIDS). This is because rule A specifically excludes SIDS from the ill-defined conditions.

What is the difference between ICD-10 and ICD-10CM?

ICD-10 is used for mortality (death) data while ICD-10-CM is used for morbidity (disease) data from the inpatient and outpatient records and physician offices. There are no plans for implementing ICD-10-CM at this point.

How do I obtain a copy of ICD-10?

Electronic and bound versions can be purchased from WHO; however, NCHS and the United States are using a copy modified by NCHS. The NCHS version converts the English spellings to American spellings and incorporates changes made after the WHO version was published. A WHO copyright bars NCHS from distributing the version being used in the U.S. The various lists of causes used to publish mortality data are available at ftp://ftp.cdc.gov/pub/health_statistics/NCHS/publications/ICD10. For more information about the ICD-10, go to: http://www.cdc.gov/nchs/icd9.htm

Change 2: Implementation of the new standard population for age-adjusting death rates

Age-adjusting is a process by which the age composition of a population is held constant so that changes or differences in age composition can be eliminated from the analysis. This is necessary because older populations have high death rates merely because death rates increase with age. Age-adjusting allows the researcher to make meaningful comparisons over time and among groups in the risk of mortality.

Since 1943, NCHS had used the 1940 U.S. population as the standard, and other agencies had used this or other populations for age-adjusting. For example, the 1970 U.S. population was used for cancer rate age-adjusting. The reason for the adoption of a new standard is to promote uniformity and comparability of data from many organizations by choosing a single population standard.

What are the effects of changing to the Year 2000 standard?

The new standard is based on the year 2000 population and begins with data year 1999. Implementation of the year 2000 standard will reduce confusion among data users and the burden on state and local agencies. Use of the year 2000 standard will also result in age-adjusted death rates that are substantially larger than those based on the 1940 standard. Further, use of the new standard will affect trends in age-adjusted rates for certain causes of death and will narrow race differentials in age-adjusted death rates.

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Why will changing to the Year 2000 standard have such effects?

This is because the age structures of the 1940 and year 2000 populations differ. From 1940 to year 2000, the U.S. population "aged" considerably. This occurred for two reasons: Fertility declined and age-specific death rates declined, particularly among the elderly population, resulting in greater survival at older ages. Figure 1 shows population pyramids for the 1940 U.S. population and the projected year 2000 U.S. population. The 1940 population is more tapered, having a wider base and narrowed tip. The year 2000 population shows a higher population concentration in the middle and older age groups, such as between 35 to 45 years of age and 65 years of age and over. Because the standard populations serve as the weights for calculating age-adjusted rates, the difference in the age structure of the populations between 1940 and year 2000 translate directly into a change in the weights used for age standardization.

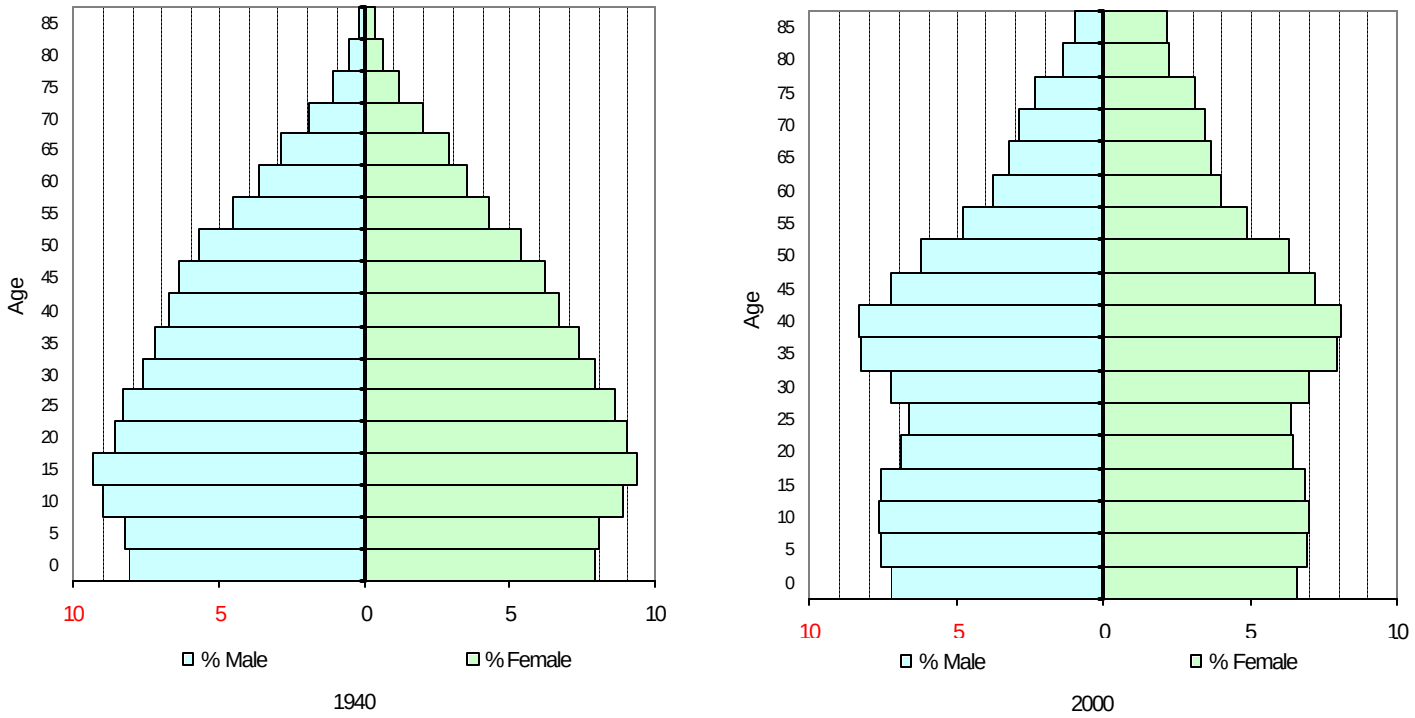
When should the age-adjusted death rate be used?

Use of age-adjusted death rates should be considered when analyzing mortality trends or comparing different population groups or different geographic areas. Crude (or unadjusted) death rates may be used to determine the absolute rate of death at any given time. Comparison of crude death rates over time and between groups/geographic areas may be misleading if the populations being compared differ in age composition.

Where can I obtain more information about the year 2000 population standard?

You may go to NCHS website at http://www.cdc.gov/nchs for additional information.

Figure1. Population pyramids for the 1940 and 2000 U.S. populations expressed as a % of total population



Acknowledgements:
This article is based on information from NCHS's 2000 Data User Conference. The author would like to thank Robert Anderson, Ph.D. Statistician, of NCHS for providing data and information for this article.

Snapshot of Davidson County Fetal and Infant Mortality Data 1989 – 1998

Editor's Note: The Division of Epidemiology has analyzed fetal and infant mortality data in Davidson County, Tennessee for the years 1989 – 1998. Preliminary results are presented below. The entire report will be released later this year.

` The fetal mortality rate in Davidson County decreased between 1992 and 1996 but increased in 1997. This increase was due in part to the increasing black fetal mortality rate. In 1998, the black fetal mortality rate was 9.7 fetal deaths per 1,000 live births plus fetal deaths in comparison to the white fetal mortality rate of 3.2 per 1,000 live births plus fetal deaths.

` In Davidson County, the fetal mortality rate stratified by age showed that maternal age greater than 35 is associated with higher rates of fetal mortality than any other age group regardless of race.

` Davidson County and Tennessee's fetal mortality rates were below that of the U.S. over the ten-year period from 1989 – 1998. However, the rates remained above the Healthy People 2000 objective of five fetal deaths per 1,000 live births plus fetal deaths.

` The three leading causes of fetal death were 1) complications associated with the placenta, umbilical cord, or membranes, 2) disorders related to short gestation/low birth weight, and 3) congenital anomalies.

` The infant mortality rate in Davidson County reached a peak of 12 infant deaths per 1,000 live births in 1993. Although the rates have decreased by 26.5% from 9.8 infant deaths per 1,000 live births in 1989 to 7.2 per 1,000 live births in 1998, they remained above the Healthy People 2000 objective of seven infant deaths per 1,000 live births.

` The disparity between white and black infant mortality rates narrowed over the 10 year period. However, the gap increased slightly in 1997 and 1998.

` Davidson County's black infant mortality rate has decreased since its peak in 1993 and remained lower than the rates for Tennessee and the U.S. in 1998.

` The neonatal mortality rate increased from 3.3 deaths per 1,000 live births in 1996 to 5.4 per 1,000 live births in 1998.

` The leading causes of neonatal deaths in 1998 were 1) short gestation/low birth weight, 2) congenital anomalies, 3) maternal complications of pregnancy, 4) infection, and 5) other respiratory conditions. The leading causes of postneonatal mortality were 1) SIDS, 2) congenital anomalies, and 3) accidents.

` Planning districts 1, 8, and 9 had the highest infant mortality rates for Davidson County, Tennessee in 1998.

Food Protection in Nashville: Then and Now

Jerry Rowland, Food Protection Division

Jerry Rowland
Director of Food Protection Division

When I was hired as a Metro Health Department food inspector in July of 1971, I received approximately one week of training prior to being placed in the field and given the responsibility of inspecting 175 establishments about once every six weeks. Back then, the inspection focused primarily on cleanliness of equipment, floors, walls, and ceilings within facilities. Industry training was virtually non-existent, so the Food Protection Division inspection staff performed solely as regulators.

A newly hired inspector today goes through nearly eight weeks of training prior to being assigned to a territory. Currently, there are approximately 320 establishments in each territory. Also, the inspector is required to enroll in and pass a national food protection certification course during the probationary period. Major emphasis of the inspection is now placed on time/temperature controls of potentially hazardous foods (hot and cold holding, cooking, re-heating and cooling-down temperatures), good hygienic practices, and cleaning and sanitization of food contact surfaces. These areas focus on the leading causes of foodborne illness in the U.S. and are related to risk factors established by the Centers for Disease Control and Prevention.

The Food Protection Division staff is involved directly with various types of food protection training as listed below:

a. Basic food protection offered in English, Chinese, and Spanish.
b. *ServSafe* (national food protection certification course).
c. *Stay Focused* (course designed to give restaurant managers the basic skills needed to inspect their own facilities).
d. *Safe at Home Plate* (short food safety presentation administered to civic and church groups, etc.).

Realizing that many children will be employed in restaurants and grocery stores in the future, the Food Protection Division developed and administers a short food protection presentation for elementary, middle, and high school students. These presentations are designed to give the student a basic knowledge of effective food protection practices. Last year, Food Protection Division inspectors' presentations reached 1,354 students.

Metro Health Department developed an awards package providing awards to restaurants that demonstrate exemplary food protection practices. This program has generated considerable interest from the food industry as well as the print and electronic media. Many restaurants have received the award, while many others continue to strive to improve and may receive the award in the near future.

The employees of the Food Protection Division strive to be accountable to the citizens of Davidson County by utilizing resources wisely. The establishment inspection load in the Food Protection Division has increased 54% since 1971, and the intensity of the inspections has increased as well. Current state law requires that each permitted establishment be inspected once each six-month period. Because some establishments pose a greater risk than others in regard to the potential for causing a foodborne outbreak, the Food Protection Division developed a risk assessment tool to assess the risk in each establishment. Assessed high-risk establishments will be inspected more frequently than those assessed as a low-risk. The Food Protection Division recently requested permission from the Tennessee Department of Health to implement a pilot risk-based inspection program for a two-year period. Hopefully, after the pilot program proves to be successful, it will be implemented fully across Davidson County resulting in a more efficient operation of the Division.

It is hoped that changes made over the past years and those planned for in the near future will allow the Food Protection Division to continue to provide exemplary food protection services for the citizens of Davidson County.

Reported cases of selected notifiable diseases for July/August 2000

Disease	Cases Reported in July/August		Cumulative Cases Reported through August	
	1999	2000	1999	2000
AIDS	43	85	107	295
Campylobacteriosis	10	4	23	26
Chlamydia	523	397	1,403	1,673
DRSP (Invasive drug-resistant *Streptococcus pneumoniae*	7	3	40	28
Escherichia coli 0157:H7	1	4	4	6
Giardiasis	8	0	20	14
Gonorrhea	445	468	1,153	1,647
Hepatitis A	5	3	36	37
Hepatitis B (acute)	3	2	11	31
Hepatitis B (perinatal)	3	1	18	13
Hepatitis C (acute)	4	0	17	12
HIV	133	68	313	328
Influenza	0	1	857	706
Neisseria meningitidis disease	0	1	4	7
Salmonellosis	13	32	40	52
Shigellosis	8	3	158	16
Syphilis (primary and secondary)	49	27	173	124
Tuberculosis	20	12	44	58
VRE (Vancomycin-resistant enterococci)	8	10	47	42

To report a notifiable disease, please contact:

Sexually transmitted diseases: Pat Petty at (615) 340-5647
Hepatitis B and C: Denise Stratz at (615) 340-2174
Vaccine-preventable diseases: Pam Trotter at (615) 340-5667
Tuberculosis: Diane Schmitt at (615) 340-5650
AIDS/HIV: Mary Angel-Beckner at (615) 340-5330
All other notifiable diseases: Pam Trotter at 340-5632